This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims

1. (currently amended): A method for detecting the presence of an enterovirus in a sample comprising the steps of:

(i) purifying contained in the sample;

(ii) reverse the RNA with primers effective to reverse transcribe enteroviral RNA to a cDNA;

(iii) contacting at least a portion of the cDNA with

(a) a composition that promotes amplification of a nucleic acid and

(b) an oligonucleotide mixture wherein the mixture comprises at least one oligonucleotide that hybridizes to a highly conserved sequence of the sense strand of an enterovirus nucleic acid and at least one oligonucleotide that hybridizes to a highly conserved sequence of the antisense strand of an enterovirus nucleic acid, wherein said mixture comprises ~~at least one oligonucleotide comprising at the 3' end thereof a sequence selected from the group consisting of~~ SEQ ID NO: 19, ~~SEQ ID NO: 20, SEQ ID NO: 21 and SEQ ID NO: 22~~;

(iv) carrying out an amplification procedure on the amplification mixture such that, if an enterovirus is present in the sample, an enterovirus amplicon is produced whose sequence comprises a nucleotide sequence of at least a portion of the VP1 gene of the enterovirus genome; and

(v) detecting whether an amplicon is present; wherein the presence of the amplicon indicates that an enterovirus is present in the sample.

2. (original) The method as described in claim 1, wherein the highly conserved sequences occur within the VP1 gene or within about 100 nucleotides from a terminus of the VP1 gene.

Claims 3-5 (cancelled)

6. (original) The method as described in claim 2, wherein at least one oligonucleotide comprises, at the 3' end thereof, a sequence that hybridizes to a sequence encoding a motif chosen from the group consisting of the sequences given by SEQ ID NO:83, SEQ ID NO:84, and SEQ ID NO:85, and at least one oligonucleotide comprises, at the 3' end thereof, a sequence that hybridizes to a sequence encoding a motif given by SEQ ID NO:86.

7. (currently amended) The method as described in claim 1, wherein the oligonucleotide mixture comprises an oligonucleotide whose sequence comprises, at the 3' end thereof, the sequence given by SEQ ID NO:22, and ~~at least one~~ an oligonucleotide ~~chosen from the group consisting of an oligonucleotide~~ whose sequence comprises, at the 3' end thereof, the sequence given by SEQ ID NO: 19~~, an oligonucleotide whose sequence comprises, at the 3' end thereof, the sequence given by SEQ ID NO:20, and an oligonucleotide whose sequence comprises, at the 3' end thereof, the sequence given by SEQ ID NO:21~~.

8. (currently amended) The method as described in claim 7, wherein the oligonucleotide mixture comprises an oligonucleotide whose sequence is given by SEQ ID NO:22, and ~~at least one~~ an oligonucleotide ~~chosen from the group consisting of an oligonucleotide~~ whose sequence is given by SEQ ID NO:19~~, an oligonucleotide whose sequence is given by SEQ ID NO:20, and an oligonucleotide whose sequence is given by SEQ ID NO:21~~.

9. (original) The method as described in claim 1, wherein the amplification procedure comprises a polymerase chain reaction.

10. (original) The method as described in claim 1, wherein the sample is chosen from the group consisting of whole blood or a fraction thereof, a bronchial wash, cerebrospinal fluid, an eye swab, a conjunctival swab, a swab or scraping from a lesion, a nasopharyngeal swab, an oral or buccal swab, pericardial fluid, a rectal swab, serum, sputum, saliva, stool, a stool extract, a throat swab, urine, brain tissue, heart tissue, intestinal tissue, kidney tissue, liver tissue, lung tissue, pancreas tissue, spinal cord tissue, skin tissue, spleen tissue, thymus tissue, cells from a tissue culture, a supernatant from a tissue culture, and tissue from an experimentally infected animal.

11. (previously presented) The method as described in claim 1, wherein the detection is carried out by a procedure chosen from the group consisting of gel electrophoresis and visualization of amplicons contained in a resulting gel, size separation matrix, capillary electrophoresis and detection of the emerging amplicon, probing for the presence of the amplicon using a labeled probe, sequencing the amplicon, and labeling a PCR primer employed in the method and detecting the label.

Claims 12-46 (cancelled)